

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2005, 12:53:59 ; Search time 6727 Seconds
(without alignments)
8650.916 Million cell updates/sec

Title: US-09-836-544B-28

Perfect score:

Sequence: 1 gggtgcaagaagagacag.....aaataagtgcacgatgacc 1201

Scoring table: IDENTITY_NUC

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

2000

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Database :

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11: gb_ats: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1201	100.0	1201	6	BD015201	BD015201 T15a cel
2	1201	100.0	1204	6	AR380482	AR380482 Sequence
3	1201	100.0	1204	6	AX697951	AX697951 Sequence
4	1201	100.0	1204	6	AX181855	AX181855 Sequence
5	1201	100.0	1204	9	HUMCD27A	M63928 Homo sapien
6	1201	100.0	1233	9	BC012160	BC012160 Homo sap
7	1199.4	99.9	1204	6	CQ721686	CQ721686 Sequence
8	1199.4	99.9	1300	6	C0865620	C0865620 Sequence
9	524	43.6	524	6	AX778265	AX778265 Sequence
10	451.8	37.6	1585	10	MUSCDD27A	L24495 Mus muscul
11	444.4	37.0	172571	9	AC006064	AC006064 Homo sapi
12	442.8	36.9	10529	9	A1504961	A1504961 Homo sap
13	442.8	36.9	26815	6	CQ865619	CQ865619 Sequence
14	441.2	36.7	140026	9	AC005840	AC005840 Homo sap
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19	249.8	20.8	2364	9	AK056500	AK056500 Homo sapi

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C	27	235.8	19.6	483	6	CQ255823	CQ255823	Sequence
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Db		61	CAGCAACTGGGCACAGAAAGAGCCGCTGGGACAGAGCAATGGCACGSCACATCCCTG	120
OY		121	GTGGGTGGCGTTCTGGGGACCCCTGGTGGGGCTCTCACTACTCCAGCCCCCAGAGCTG	180
Db		121	GTGGGTGGCGTTCTGGGGACCCCTGGTGGGGCTCTCACTACTCCAGCCCCCAGAGCTG	180
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OY		361	TAACTCTGATCTTCTGTTTGGCAATGCAACCATCACTGCAATGTGTGATGGTGGCTGGC	420
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OY		421	CAATGGCTGGCAGTGCAGAGGACAAAGAGTGCACCGAGTGTGATCCTCTTCCAAACCTTTC	480
Db		421	CAATGGCTGGCAGTGCAGAGGACAAAGAGTGCACCGAGTGTGATCCTCTTCCAAACCTTTC	480
OY		481	GCTGACCGCTGGGTGTCTCAGGCGCTTGAGCCACACCTTCAAGCCACCCACTTAACCTTA	540
Db		481	GCTGACCGCTGGGTGTCTCAGGCGCTTGAGCCACACCTTCAAGCCACCCACTTAACCTTA	540
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OY		601	GCAAGTGCCTGCCCGGACTCTCTTACCCACTGGCCACCCCAAGATCCCTGTGCAAGCTC	660
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Dd	1141	CAC TTC TCT GCT GCG AAG ACC CAC ATG CTAT CAC AG CGG G CAA AAT TAA AGT GAC GAT GAC	1200
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Dd	1201	C	1201
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DEFINITION	Sequence 1027 from patent US 6607879.	linear	PAT 18-DEC-2003
ACCESSION	AR380482		
VERSION	AR380482.1	GI:40088116	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1204)		
TITLE	Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.		
JOURNAL	Compositions for the detection of blood cell and immunological		
FEATURES	response gene expression		
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Dd	61	CAGCAACTGGGCA CAGAAAGAGCGCGCTGGGACAGGACCATGGACAGCGCACATCCCTG	120
Qy	121	GTGGCTGTGCGTTCGTGGGGAACCTGTGTGGGGCTCTCAGCTAATTCAGCCCCCAAGACTG	180
Dd	121	GTGGCTGTGCGTTCGTGGGGAACCTGTGTGGGGCTCTCAGCTAATTCAGCCCCCAAGACTG	180
Qy	181	CCCGAAGAGCACTACTGCGGCTCAGGGAAGCTGTGCTGCCAATGTGTAGACCAAGAAC	240
Dd	181	CCCGAAGAGCACTACTGCGGCTCAGGGAAGCTGTGCTGCCAATGTGTAGACCAAGAAC	240
Qy	241	ATTCTCGTGAAGGACTGTGACCGACGATPAGAAAGGCTGTCAAGTGTATCTTTCATATAC	300
Dd	241	ATTCTCGTGAAGGACTGTGACCGACGATPAGAAAGGCTGTCAAGTGTATCTTTCATATAC	300
Qy	301	GGGGGTCTCCTTCTCTCCTGACCAACACCCGGGCCCACTGTGAGACTGTGGCACTG	360
Dd	301	GGGGGTCTCCTTCTCTCCTGACCAACACCCGGGCCCACTGTGAGACTGTGGCACTG	360
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Dd	361	TAACTCTGTGTTCTTGTTGGCAATGCAATATACCTGCCAATGTGATGTGCTGTG	420
Qy	421	CAATGGCTGGAGTGCAGGGGCAAGAGTGTGACCCGAGTGTGATCTCTTCCAAACCTTC	480
Dd	421	CAATGGCTGGAGTGCAGGGGCAAGAGTGTGACCCGAGTGTGATCTCTTCCAAACCTTC	480
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Dd	481	GCTTACCGCTGTGCTGTCTGAGGCGCTGAGCCCAACCTCTAGGCCCAACCACTTACTT	540
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ACCESSION	AX697951											
VERSION	AX697951.1	GI:29499010										
KEYWORDS												
SOURCE												
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
REFERENCE	1	Lucas, J., Dialynas, D. and Briggs, K.										
AUTHORS	Agonists and antagonists of modulator for use in the treatment of											
TITLE	metabolic disorders											
JOURNAL	Patent: WO 03009862-A 1 06-FEB-2003;											
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OY	181	CCAGAGAGGCACTACTAGGCTCAAGGAAAGCTGTGCTCCAGATGTGTAGGACAGGAAC	240	
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DB	361	TAACTCTGATCTTCTGTTGGCAATGCAACCATCACTGCCAATGCTGATGTGCTGTG	420	
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RESULT 4

AX818155

LOCUS AX818155 1204 bp DNA linear PAT 10-DEC-2003

DEFINITION Sequence 26 from Patent WO03068268.

ACCESSION AX818155

VERSION AX818155.1 GI:39723234

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human); Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

Ek, S., Borrebaeck, C.A. and Bhinger, M.
Treatment outcome, diagnosis and imaging of disease

Patent: WO 03068268-A 26 21-AUG-2003;

BIOINVENT INTERNATIONAL AB (SE)

Location/Qualifiers

FEATURES

source

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ORIGIN

Query Match 100.0%; Score 1201; DB 6; Length 1204;
Best Local Similarity 100.0%; Pred. No. 3.2e-281;
Matches 1201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGGGTGCAAAAGAGACAGACGCGCCAGCTTGAGGTGCTAACTCCAGAGGCCAGAT 60
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HUMCD27A

LOCUS HUMCD27A

DEFINITION Homo sapiens T cell activation antigen (CD27) mRNA, complete cds.

ACCESSION M63928.1

VERSION M63928.1

KEYWORDS T-cell activation antigen CD27.

1204 bp mRNA linear PRI 31-DEC-1994
T-cell activation antigen CD27.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Camerini, D., Walz, G., Loenen, W.A., Bors, J., and Seed, B.
 TITLE The T cell activation antigen CD27 is a member of the nerve growth
 factor/tumor necrosis factor receptor gene family
 JOURNAL J. Immunol. 147 (9), 3165-3169 (1991)
 MEDLINE 92033149
 PUBMED 1655907
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 VERSION BC012160.1 GI:15082490
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
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 REFERENCE 1 (bases 1 to 1323)
 AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hale, L.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Phay, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1323)
Strausberg, R.
Direct Submission
Submitted (02-Aug-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Mabson, Mike R. Mayo, Josh Moran, Ryan Morin, Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabh, Parvaneh Saeedi, JR Santos, Angeliq Schnerch, Ursula Skalska, Duane Smallus, Jeff Stott, Miranda Teal, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAL Plate: 29 Row: h Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3,2e-281;
Matches 1201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION CQ721686.1 GI:42282543
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of humenexons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 7620 06-SEP-2002;
PE Corporation (NY) (US)

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Matches 1200; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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VERSION C0869620.1 GI:51999481
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REFERENCE 1
AUTHORS Morris, D.W., Morris, D.W. and Malandro, M.S.
TITLE Novel therapeutic targets in cancer
JOURNAL Patent: WO 2004074320-A 41 02-SEP-2004;
Sagres Discovery, Inc. (US)

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901 CTGCACTACAGGCTGTGCTCTCAGCCCAACCCCGGAGGAGTGTGATCAGAAAGAGGAGTGTGATCAG 960
998 CTGCACTACAGGCTGTGCTCTCAGCCCAACCCCGGAGGAGTGTGATCAGAAAGAGGAGTGTGATCAG 1057

ORIGIN

961 TGGCAGCCCAACCTGAGTCCCATCTCTGTCAAGGAGCCCTTCTCTGTATACGCTGACA 1020
1058 TGGCAGCCCAACCTGAGTCCCATCTCTGTCAAGGAGCCCTTCTCTGTATACGCTGACA 1117
1021 GAGTGTCTTTTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
1118 GAGTGTCTTTTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1177
1081 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
1178 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1237
1141 CACTTCTGTCTCTGAAAGAGCCAGATGTCTACAGAGCGGCAAAATTAAGTGCAGATGAC 1200
1238 CACTTCTGTCTCTGAAAGAGCCAGATGTCTACAGAGCGGCAAAATTAAGTGCAGATGAC 1297
1201 C 1201
1298 C 1298

RESULT 9
AX778265 524 bp DNA linear PAT 14-JUL-2003
LOCUS AX778265
DEFINITION Sequence 422 from Patent WO03039443.
ACCESSION AX778265
VERSION AX778265.1 GI:32695259
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Haeferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnitzger, S.,
Dugas, M., Eils, R., Brots, B., and Mergenthaler, S.
TITLE Novel genetic markers for Leukemia
JOURNAL Patent: WO 03039443-A 422 15-MAY-2003;
Deutsches Krebsforschungszentrum (DKFZ);
Ludwig-Maximilians-Universitaet Muenchen (LMU); Haeferlach, Torsten,
PD Dr. Dr. Schoch, Claudia (DE); Kern, Wolfgang (DE)

FEATURES
source 1. .524
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ORIGIN

Query Match 43.6%; Score 524; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.7e-116;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

649 CCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 708
1 CCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 60
709 CACCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 768
61 CACCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 120
769 AAGTCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 828
121 AAGTCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 180
829 CACCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 888
181 CACCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 948
889 CACCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 900
241 CACCTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 960
949 GAGAGTGTGAGCTCCGATTTTATTTGATCTCTGTGATCTTCTGTGATGTTCTTGTGTTT 1008


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Db      301 GAGAGGAGACCTGGGAGGACCAACTGCACTGCCATCCCATCTCTTGTCAAGGGCCCTTCTCTG
Qy      1009 GTACACGTGACAGAGTGCCTTTTTCAGAGACTGCGACGGAGAGACAATATGTATAGT 1068
Db      361 GTACACGTGACAGAGTGCCTTTTTCAGAGACTGCGACGGAGAGACAATATGTATAGT 420
Qy      1069 GGAAGACTGGGAACAGAGCCGACGAGCTGCCTGCGCTGAGAGAGGGCGGGGCTCT 1128
Db      421 GGAAGACTGGGAACAGAGCCGACGAGCTGCCTGCGCTGAGAGAGGGCGGGGCTCT 480
Qy      1129 GGTGTAAACACACTTCTCTGTCGAAAGAACCCACATGCTACA 1172
Db      481 GGTGTAAACACACTTCTCTGTCGAAAGAACCCACATGCTACA 524

RESULT 10
MUSCD27A
LOCUS      MUS musculus CD27 antigen (Cd27) mRNA.
ACCESSION  L24495.1 GI:403146
VERSION     CD27 antigen.
KEYWORDS    Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 1585)
REFERENCE   Gravesstein, L.A., Blom, B., Noltén, L.A., de Vries, E., van der
            Horst, G., Ossendorp, F., Boret, J., and Loenen, W.A.
            Cloning and expression of murine CD27: comparison with 4-1BB,
            another lymphocyte-specific member of the nerve growth factor
            receptor family
            Eur. J. Immunol. 23 (4), 943-950 (1993)

JOURNAL     93209296
MEDLINE     8384562
PubMed      8384562
COMMENT     Original source text: Mus musculus (strain B6/CBAF1J) (library:
            oligo dt in lambda ZAP) female juvenile, 6-8 weeks thymus cDNA to
            mRNA.

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                    /sex="female"
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                    /tissue_1ib="oligo dt in lambda ZAP"

ORIGIN
Query Match      37.6%; Score 451.8; DB 10; Length 1585;
Best Local Similarity 73.2%; Pred. No. 5.2e-99;
Matches 633; Conservative 0; Mismatches 202; Indels 30; Gaps 3;

Qy      69 GGGGACAGAAAGAGCGCGCTGGGAGGAGACATGAGACGGCCACATCCCTGGTGTGT 128
Db      146 GGGGCTCAGAAAGATCTCCCTGGGAGGAGACTATGAGTGGCCACCTCCCTACTGGCTCT 205
Qy      129 GCGTTCTGGGAGCCCTGGTGGGGCTCTCAGCTCTCAGCGCCCAAGAGGCTGCCAGAGA 188
Db      206 GCATGCTGGGAGCCTTGTGTGAGACTCTCAGCTACCTTACGCCCAAGAGGCTGTCCAGACA 265
Qy      189 GGCACACTAGTGGGCTCAGGAAAGCTGTCTGCCAGATGTGTGAGCCAGAACTTCTCG 248
Db      266 AACACTACTGAGACTGGGGAGAGACTGTGCTGCCGAGATGTGTGAGCCAGTATCAATTTCTTG 325
Qy      249 TGAAGACCTGTGACACGATAGAAAGCTCTCAGTGTATCTTGTGATACCGGGGCTCT 308
Db      326 TGAAGACCTGTGAGACAGAGAAACACACTCTCAGTGTATCTTGTATACAGGACCT 385
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Db      386 CCTTCTCTCAGACTACACACCCGGCCCACTGAGAGACTGACGATGTAACTCTG 445
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Db      446 GTTTCCTTATCCGCACTGACAGTCACTGACCAATGTCTAGTGTGACACTGTTCMAAAGCT 505
Qy      429 GGCAGTGCAGGGGCAAGAGAGTGCACCGAGTGTGATCTCTTCCAAACCTTCGCTGACCG 488
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Qy      549 AGATGCTGAGAGCCAGAGACAGTGGGCAATGCACTGTGGCTGACTTCAAGCACTGC 608
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Qy      609 CTGCCCCGACTCTCTTACCCCACTGGGCAACCCCAAGATCCCTGTGACCTCCGATTTTA 668
Db      659 CCAACTGCACTGTCTATAGCCAGCGGTATCCCATAGACCCCTGTGACAGCTGGACTGCA 718
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Db      779 TCTTCATCAAGAGAAATATATGATCAACAAAGAGAAAGTCTGTGAGACCTGCGAAG 835
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Db      956 ACAGAGGGCCATCCACAGAGACTCT 980

RESULT 11
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LOCUS      Homo sapiens 12 PAC RP5-940U5 (Roswell Park Cancer Institute Human
ACCESSION  AC006064 complete sequence.
VERSION     AC006064.10 GI:28191361
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
            1 (bases 1 to 172571)
REFERENCE   1 (bases 1 to 172571) bp
            Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
            Alsbrooks, S.L., Amaralunga, H.C., Are, J.R., Ayele, M., Banks, T.,
            Barbarta, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
            Bouck, J., Bowls, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P.,
            Buhay, C., Burch, P., Burkett, C., Butrell, K.L., Byrd, N.C.,
            Carron, T.P., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
            Chen, G., Chen, R., Chen, Z., Chin, D., Chowdhury, I., Christopoulos, C.,
            Cleveland, C.D., Cox, C., Coyle, M.D., Dathenbury, S.R., David, R.,
            Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
            Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
            Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
            Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S.,
            Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P.,
            Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N.,
            Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
            Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlik, P.,
            Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M.,

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Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulik, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kravovic, J., Kureishi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichcharee, C., Lien, C., Liu, U., Liu, W., Louised, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maneswar, M., Mapu, P., Maronde, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzner, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwona, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, D., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoochert, N., Sison, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tamsey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vaquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kuchelapatti, R., Weinstock, G., and Gibbs, R.

TITLE
Unpublished

JOURNAL
2 (bases 1 to 172571)

REFERENCE
Worley, K.C.

AUTHORS
Direct Submission

TITLE
Submitted (26-NOV-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL
3 (bases 1 to 172571)

REFERENCE
Worley, K.C.

AUTHORS
Direct Submission

TITLE
Submitted (07-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL
4 (bases 1 to 172571)

REFERENCE
Worley, K.C.

AUTHORS
Direct Submission

TITLE
Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL
5 (bases 1 to 172571)

REFERENCE
Worley, K.C.

AUTHORS
Direct Submission

TITLE
Submitted (01-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL
On Feb 1, 2003 this sequence version replaced gi:4572650.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

FEATURES

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SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality/info/genbank.annotation.html>.

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Query Match 36.9%; Score 442.8; DB 9; Length 10529;
Best Local Similarity 99.6%; Pred. No. 5.8e-97;
Matches 444; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 756 CAAACAAAGAGAAAGTCTGTGAGACCTGACGACCTTGTCTTACAGCTGCCAGG 815
DB 8151 CAGACAAAGAGAAAGTCTGTGAGACCTGACGACCTTGTCTTACAGCTGCCAGG 8210
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DB 8211 AGGAGAGGGACGACACCATCCCATCCAGAGATTAACGAATAACGAGCCTGCTGT 8270
QY 876 CCCCTGAGCAGACCTGCGGTAGCTGACCTACAGCCCTGACCTCCACCCCGC 935
DB 8271 CCCCTGAGCAGACCTGCGGTAGCTGACCTACAGCCCTGACCTCCACCCCGC 8330
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QY 996 GGCCCTTCTCTGTACAGTGAAGAGTGCCTTTTCAGACTGGCAGGAGAGACAA 1055
DB 8391 GGCCCTTCTCTGTACAGTGAAGAGTGCCTTTTCAGACTGGCAGGAGAGACAA 8450
QY 1056 ATATGATGAGGTGAGAGTGGAGACGAGACCCAGCCAGCTGCGCTGCGAGGA 1115

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Db      8451 ATATGATGAGGTGGAGAGTGGAGAGGAGCCAGCTGCGCTGCGTGGAGGA 8510
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Db      8511 GGGCGGGGGGCTCTGCTTTGTAACACACTTCTGCTGCGGAAAGCCACATGCTACAGA 8570
QY      1176 GGGGCAAAATTAAGTGCAGATGACC 1201
Db      8571 GGGGCAAAATTAAGTGCAGATGACC 8596

RESULT 13
LOCUS   C0869619 26815 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 40 from Patent WO2004074320.
ACCESSION C0869619
VERSION   C0869619.1 GI:51999480
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Morris,D.W., Morris,D.W. and Malandro,M.S.
TITLE    Novel therapeutic targets in cancer
JOURNAL  Patent: WO 2004074320-A 40 02-SEP-2004;
           Sagres Discovery, Inc. (US)
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ORIGIN
Query Match 36.9%; Score 442.8; DB 6; Length 26815;
Best Local Similarity 99.6%; Pred. No. 5e-97;
Matches 444; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      756 CAAACAAAGAGAAAGTCTGTGAGAGCTTGCAAGCTTGTCTTACAGCTGCCCAAGG 815
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Db      16427 AGAGAGAGGGACACATCCCATCCAGAGAGATTACGAAACCGAGACCTGCTGCT 16486
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QY      996 GGGCCCTTCTGTGTACCTGACAGTGTCCCTTTTGGACATGGAGGAGGAGAGCA 1055
Db      16607 GGGCCCTTCTGTGTACCTGACAGTGTCCCTTTTGGACATGGAGGAGGAGAGCA 16666
QY      1056 ATATGATGAGGTGGAGAGTGGAGAGGAGCCAGCTGCGCTGCGTGGAGGA 1115
Db      16667 ATATGATGAGGTGGAGAGTGGAGAGGAGCCAGCTGCGCTGCGTGGAGGA 16726
QY      1116 GGGCGGGGGGCTCTGCTTTGTAACACACTTCTGCTGCGGAAAGCCACATGCTACAGA 1175
Db      16727 GGGCGGGGGGCTCTGCTTTGTAACACACTTCTGCTGCGGAAAGCCACATGCTACAGA 16786
QY      1176 GGGGCAAAATTAAGTGCAGATGACC 1201
Db      16787 GGGGCAAAATTAAGTGCAGATGACC 16812

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RESULT 14

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AC005840/c
LOCUS   AC005840 140026 bp DNA linear PRI 20-OCT-2000
DEFINITION Homo sapiens complete sequence of a PAC clone RPL-102E24 containing
           SYB1, CD27, and SCNN1A genes.
ACCESSION AC005840
VERSION   AC005840.2 GI:10938025
KEYWORDS  HTG.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Montgomery,K.T., Lau,S.T. and Kucherlapati,R.
TITLE    High Throughput Sequencing of Human Chromosome 12
JOURNAL  Unpublished
           2 (bases 1 to 140026)
REFERENCE
AUTHORS  Montgomery,K.T., Lau,S.T. and Kucherlapati,R.
TITLE    Direct Submision
JOURNAL  Submitted (22-OCT-1998) Department of Molecular Biology, Albert
           Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY
           10461, USA
           3 (bases 1 to 140026)
           10461, USA
           10461, USA
           3 (bases 1 to 140026)
           Montgomery,K.T., Lau,S.T. and Kucherlapati,R.
           Direct Submision
           Submitted (20-OCT-2000) Department of Molecular Genetics, Albert
           Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY
           10461, USA
           On Oct 20, 2000 this sequence version replaced gi:3779004.
           -----Genome Center:
           Albert Einstein College of Medicine
           Code: AECOM
           Web site: http://sequence.aecom.yu.edu/chr12/
           Contact: jhan@sequence.aecom.yu.edu

COMMENT

```

CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human sequences.

Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA sequences in Unigene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Attempts are made to complete double stranded sequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the annotation as Low Coverage. Low coverage linkages are verified by PCR product size verification or verification of forward and reverse reads from clones which span the low coverage area.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameter. Regions that do not meet this requirement are annotated as Low Quality.

-----Summary Statistics
Center project name: RPL-102E24
Sequencing vector: M13
Chemistry: Dye-terminator Big Dye; 100%
Assembly program: Phrap version 0.990119
Contig length: 140026
Fraction of Phrap value < 40: 0.0426
Error Rate in Consed: 0.56 per 10,000 bases
Number of N's in consensus: 1

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